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## Erratum

### The murky origins of the coronavirus SARS-CoV-2, the causative agent of the COVID-19 pandemic

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Figure 2 corrected to provide the correct template of SARS-CoV-2 sequence accession number and the correct residue numbering.

Coronavirus/seq no(SARS-CoV-2)	671											681				686				
Bat RmYN01(AGC74176.1)	C	A	S	Y	H	T	A	S	-	L	L	-	-	-	-	R	N	T	G	Q
Bat RaTG13(QHR63300.2)	C	A	S	Y	Q	T	Q	T	N	S	-	-	-	-	-	R	S	V	A	S
SARS-CoV-2(P0DTC2.1)	C	A	S	Y	Q	T	Q	T	N	S	-	P	R	R	A	R	S	V	A	S
SARS-CoV-1(P59594)	C	A	S	Y	H	T	V	S	-	L	L	-	-	-	-	R	S	T	S	Q
MERS(K9N5Q8)	C	A	L	P	D	T	P	S	T	L	T	P	R	S	V	R	S	V	P	G
Human 229E(P15423)	C	A	D	G	S	I	I	A	V	Q	-	P	R	N	V	-	S	Y	D	S
Human NL63(Q6Q1S2)	C	A	D	G	S	L	I	P	V	R	-	P	R	N	-	S	S	-	D	N
Human HKU1(Q0ZME7)	C	I	D	Y	A	L	P	S	S	-	-	R	R	K	R	R	G	I	S	S
Human OC43(P36334)	C	V	D	Y	S	K	N	-	-	-	-	R	R	S	R	G	A	I	T	T

**Figure 2.** Comparison of the spike protein segment containing the furin cleavage site across viruses specific for bat and human hosts. The top two rows are bat sequences. The middle three are the agents of severe human disease. The last four rows are sequences from the coronaviruses generally causing relatively mild respiratory infections. The blue colour rows highlight the identity of the segments flanking the furin cleavage site in the virus responsible for COVID-19 and a bat virus. Residues conserved at the furin cleavage site (681–686) are highlighted in yellow.